



Exhibit A
C mparison SEQ ID NO:4 vs. IPI00044749.2

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000
Please cite:
W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAAxJayWj: 1214 aa
>seqid4
vs /tmp/fastaDAayJayWj library
searching /tmp/fastaDAayJayWj library

1258 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 40, opt: 28, gap-pen: -12/-2, width: 16
Scan time: 0.066
The best scores are: opt
IPI00044749.2

(1258) 4775

>>IPI00044749.2

(1258 aa)

initn: 4773 initl: 4773 opt: 4775
Smith-Waterman score: 7822; 96.343% identity in 1258 aa overlap (1-1214:1-1258)

	10	20	30	40	50	60
seqid4	MEKYVRLQKIGEGSFGKAILVKSTEDGRQYVIKEINISRMSSKEREESRREVAVLNMKH					
IPI000	MEKYVRLQKIGEGSFGKAILVKSTEDGRQYVIKEINISRMSSKEREESRREVAVLNMKH					

	10	20	30	40	50	60
seqid4	PNIVQYRESFEENGSLYIVMDYCEGGDLFKRINAQKGVLFQEDQILDWFWVICLALKVHV					
IPI000	PNIVQYRESFEENGSLYIVMDYCEGGDLFKRINAQKGVLFQEDQILDWFWVICLALKVHV					

	70	80	90	100	110	120
seqid4	DRKILHRDIIKSNIFLTKDGTVQLGDFGIARVLNSTVELARTCIGTPPYLSPEICENKPY					
IPI000	DRKILHRDIIKSNIFLTKDGTVQLGDFGIARVLNSTVELARTCIGTPPYLSPEICENKPY					

	130	140	150	160	170	180
seqid4	NNKSDIHWALGCVLYELCTLKHAFAEAGSMKNLVLKIISGSFPPVSLHYSYDLRSIVLSQLFK					
IPI000	NNKSDIHWALGCVLYELCTLKHAFAEAGSMKNLVLKIISGSFPPVSLHYSYDLRSIVLSQLFK					

	190	200	210	220	230	240
seqid4	RVNPRDRPSVNSILEKGFIAKRIEKLFLSQLIAEEFCLKTFKFGSQPIPAKRPASGQNSI					
IPI000	RVNPRDRPSVNSILEKGFIAKRIEKLFLSQLIAEEFCLKTFKFGSQPIPAKRPASGQNSI					

	250	260	270	280	290	300
seqid4	SVMPAQKITKPAKYGIPLAYKKYGDKKLHEKKPLQKHQAHQTPKEKRVNTGEERRKISE					
IPI000	SVMPAQKITKPAKYGIPLAYKKYGDKKLHEKKPLQKHQAHQTPKEKRVNTGEERRKISE					

	310	320	330	340	350	360
seqid4	SVMPAQKITKPAKYGIPLAYKKYGDKKLHEKKPLQKHQAHQTPKEKRVNTGEERRKISE					
IPI000	SVMPAQKITKPAKYGIPLAYKKYGDKKLHEKKPLQKHQAHQTPKEKRVNTGEERRKISE					

	310	320	330	340	350	360
seqid4	SVMPAQKITKPAKYGIPLAYKKYGDKKLHEKKPLQKHQAHQTPKEKRVNTGEERRKISE					
IPI000	SVMPAQKITKPAKYGIPLAYKKYGDKKLHEKKPLQKHQAHQTPKEKRVNTGEERRKISE					

```

IPI000 SVMPAQKITKTPAAKYGIPLAYKKYGDKKLHEKKPLQKHQAQHTPEKRVNTGEERRKISE
      310      320      330      340      350      360
seqid4      370      380      390      400      410      420
EAAKRRRLFIEKEKKQKDQIISLMKAEQMQRQEKERLERINRARBQGWNRVLSAGSGSE
IPI000 EAAKRRRLFIEKEKKQKDQIISLMKAEQMQRQEKERLERINRARBQGWNRVLSAGSGSE
      370      380      390      400      410      420
seqid4      430      440      450      460      470
VKAPFLGSGGTIAPSSFSRRGQYEHYHAIFDMQQQRAEDNEAKWKREIYGRGLPER--
      430      440      450      460      470      480
IPI000 VKAPFLGSGGTIAPSSFSRRGQYEHYHAIFDMQQQRAEDNEAKWKREIYGRGLPERGIL
      430      440      450      460      470      480
seqid4 -----
      480      490
-----QKGQLAVERAKQVEEFLQR
      490      500      510      520      530      540
IPI000 PGVRPGFFYGAAGHHHFPDADDIRKTLKRLKAVSKQANANRQKQLAVERAKQVEEFLQR
      490      500      510      520      530      540
seqid4      500      510      520      530      540      550
KREAMQNKARAEGHMVYLARLRQIRLQNFNERQQIKAKLRGEKKAEANHSEQGEGSEADM
IPI000 KREAMQNKARAEGHMVYLARLRQIRLQNFNERQQIKAKLRGEKKAEANHSEQGEGSEADM
      550      560      570      580      590      600
seqid4      560      570      580      590      600      610
RRKKIESLKAHANARAVALKEQLERKRKEAYEREKKVWEHLVAKGVKSSDVSPPLGQHE
IPI000 RRKKIESLKAHANARAVALKEQLERKRKEAYEREKKVWEHLVAKGVKSSDVSPPLGQHE
      610      620      630      640      650      660
seqid4      620      630      640      650      660      670
TGGSPSKQMRSVISVTSALKKEVGVDSSLTDTRETSEEMQKTNNAISSKREILRLNLNL
IPI000 TGGSPSKQMRSVISVTSALKKEVGVDSSLTDTRETSEEMQKTNNAISSKREILRLNLNL
      670      680      690      700      710      720
seqid4      680      690      700      710      720      730
KAQEDEKGMQNLSDTFEINVHEDAHEHEKEKSVSSDRKKWEAGGQLVPLDELTLDTSTS
IPI000 KAEDEKGMQNLSDTFEINVHEDAHEHEKEKSVSSDRKKWEAGGQLVPLDELTLDTSTS
      730      740      750      760      770      780
seqid4      740      750      760      770      780      790
TTERHTVGVEIKLPGNSPRRAWGKSPTDSVLKILGEAELQLQTELENTTIRSEISPEG
IPI000 TTERHTVGVEIKLPGNSPRRAWGKSPTDSVLKILGEAELQLQTELENTTIRSEISPEG
      790      800      810      820      830      840
seqid4      800      810      820      830      840      850
EKYKPLITGEKKVQCISHEINPSAIVDSPVETKSPFSEASQMSLKEGNNLEEPDLET
IPI000 EKYKPLITGEKKVQCISHEINPSAIVDSPVETKSPFSEASQMSLKEGNNLEEPDLET
      850      860      870      880      890      900
seqid4      860      870      880      890      900      910
EILQEPSGTNKLDESPLCTIPDVIWISSEKETKETQSADRITIQENEVSEDGVSSTVDQLSD

```

```

IPI000 EILQEPGSGNKDESLPCTITDWWIVSEKKETKTKQSADRITIQENEVSEIDGVSSVTDQLSD
          910          920          930          940          950          960
seqid4  IHIEPGTNDQSQHSKCDVDKSVQPEPFPHKVHSEHLNLPVQVQSVCSPSESFAPRSHSH
          .....
IPI000 IHIEPGTNDQSQHSKCDVDKSVQPEPFPHKVHSEHLNLPVQVQSVCSPSESFAPRSHSH
          970          980          990          1000          1010          1020
seqid4  LPPKNKNKNSLLIGLSTGLFDANNPKMLRTCSLDPLSKLFRITLMDVPVTVGDVRQDNLEID
          .....
IPI000 LPPKNKNKNSLLIGLSTGLFDANNPKMLRTCSLDPLSKLFRITLMDVPVTVGDVRQDNLEID
          1030          1040          1050          1060          1070          1080
seqid4  EKDENIKEGPSDSSEDIVFEETDTDLQELQASMEQLLRQPGGEYSVEEESVLKNSDVEP
          .....
IPI000 ETEDENIKEGPSDSSEDIVFEETDTDLQELQASMEQLLRQPGGEYSVEEESVLKNSDVEP
          1090          1100          1110          1120          1130          1140
seqid4  TANGTDAVEDDNPSSSALNEEWHSDNSDGEIASSECDVSFNHLEELRLHLEQEMGFE
          .....
IPI000 TANGTDAVEDDNPSSSALNEEWHSDNSDGEIASSECDVSFNHLEELRLHLEQEMGFE
          1150          1160          1170          1180          1190          1200
seqid4  KFFEVYEEKIAIHEDENITEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE
          .....
IPI000 KFFEVYEEKIAIHEDENITEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE
          1210          1220          1230          1240          1250

```